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MYCOBIOTA AND MYCOTOXIN CONTENT OF MAIZE COLLECTED FROM WAREHOUSES IN SOUTHERN HUNGARY AND VOJVODINA IN 2012

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Maize is one of the most important ingredients of feed formulations worldwide. Southern Hungary and Vojvodina share the same climatic conditions, which are highly favorable for maize production. Several fungal pathogens are able to infect maize, and their mycotoxins may cause various disease symptoms.
The aims of our studies were to examine the mycobiota and mycotoxin contamination of maize hybrids after storage to get insight into their effects on animal welfare. Altogether 20 samples were collected from various warehouses and outlets in the region. Surface-sterilized maize seeds were placed on dichloran-rose bengal selective media, and the isolated fungal strains were identified using morphological and sequence-based methods. Maize seeds were disinfected with 70% ethanol. 50 seeds were placed onto plates containing a selective medium, and incubated at 25°C for 7 days. After the incubation time we examined the percentage of fungal infection of the maize grains. The fungal colonies were isolated and maintained on malt extract agar slants.
Among the Hungarian samples, the lowest fungal infection was 20% in the case of a maize sample from Csanádpalota. Fungal contamination of maize sample from Kiszombor was 40%, while 50-50% infection rates were detected for samples two other samples collected in Csanádpalota and Mihályteleki. We found 60-60% infected seeds for maize samples from Mezőhegyes, Tiszasziget and Algyő. The highest fungal contamination was 80% in the case of a maize sample from Szentes.
Regarding the Serbian samples, the most heavily contaminated samples were Becsej NS640, Ruma NS 72 and Panchevo-Poncho respectively. All of the examined seeds were contaminated by fungi. The lowest observed fungal infection was 56% in the case of the Pionir PR 35F38 sample.
Among the isolated fungi the predominant species were members of the genus *Aspergillus*, followed by *Penicillium* and *Fusarium* species.
The potentially aflatoxin producing *Aspergillus flavus* species dominated in the samples (11/28 isolates). *Penicillium*, *Trichoderma*, *Bionectria*, *Arthrinium*

species and the fumonisin producing *Fusarium verticillioides* were also identified.

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